



SEQUENCE LISTING

110> La Jolla Institute for Allergy and Immunology
Ware, Carl F.

<120> LIGAND FOR HERPES SIMPLEX VIRUS ENTRY
MEDIATOR AND METHODS OF USE

<130> 051501-0276397

<140> 09/549,096

<141> 2000-04-12

<150> 08/898,234

<151> 1997-07-30

<150> 60/051,964

<151> 1997-07-07

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Forward primer sequence

<400> 1

cggagatctg agttcatcct gctagctgg

29

<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Backward primer sequence

<400> 2

ataggatccc ttggtctggt gctgacattc c

31

<210> 3
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Forward primer sequence

<400> 3

gacgtcagat cttccacact ttctccta 29

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Backward primer sequence

<400> 4

gaacagagat ctcattgctc ctggctctg 29

<210> 5
 <211> 1169
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)..(771)

<400> 5
 gaggttgaag gacccaggcg tgtcagccct gctccagaga ccttgggc atg gag gag 57
 Met Glu Glu
 1

agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc 105
 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile
 5 10 15

cca ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg 153
 Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser Cys Ser Val
 20 25 30 35

gcc cgg gtg ggt ctg ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg 201
 Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Leu Met Gly Ala Gly Leu
 40 45 50

gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag 249
Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu
55 60 65

atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg 297
Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu
70 75 80

ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca 345
Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr
85 90 95

ggg gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag 393
Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu Leu Trp Glu
100 105 110 115

act cag ctg ggc ctg gcc tcc ctg agg ggc ctc agc tac cac gat ggg 441
Thr Gln Leu Gly Leu Ala Ser Leu Arg Gly Leu Ser Tyr His Asp Gly
120 125 130

gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg 489
Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
135 140 145

cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc 537
Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
150 155 160

cac ggc ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg 585
His Gly Leu Tyr Lys Arg Thr Pro Arg Tyr Pro Glu Glu Leu Glu Leu
165 170 175

ttg gtc agc cag cag tca ccc tgc gga cgg gcc acc agc agc tcc cgg 633
Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser Ser Ser Arg
180 185 190 195

gtc tgg tgg gac agc agc ttc ctg ggt ggt gtg gta cac ctg gag gct 681
Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His Leu Glu Ala
200 205 210

ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg 729
Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
215 220 225

cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga 771
Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
230 235 240

aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag aggggtgcctc 831

aggggaaaga aaactcacga agcagaggct gggcgtggtg gctctcgcct gtaatcccag 891

cactttggga ggccaaggca ggcggatcac ctgagggtcag gagttcgaga ccagcctggc 951

taacatggca aaaccccatc tctactaaaa atacaaaaat tagccggacg tgggtggtgcc 1011

tgccctgtaat ccagctactc aggaggctga ggcaggataa ttttgcttaa acccgaggagg 1071
 cggaggttgc agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga 1131
 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1169

<210> 6
 <211> 240
 <212> PRT
 <213> Homo sapien

<400> 6

Met	Glu	Glu	Ser	Val	Val	Arg	Pro	Ser	Val	Phe	Val	Val	Asp	Gly	Gln	1	5	10	15
Thr	Asp	Ile	Pro	Phe	Thr	Arg	Leu	Gly	Arg	Ser	His	Arg	Arg	Gln	Ser	20	25	30	
Cys	Ser	Val	Ala	Arg	Val	Gly	Leu	Gly	Leu	Leu	Leu	Leu	Leu	Met	Gly	35	40	45	
Ala	Gly	Leu	Ala	Val	Gln	Gly	Trp	Phe	Leu	Leu	Gln	Leu	His	Trp	Arg	50	55	60	
Leu	Gly	Glu	Met	Val	Thr	Arg	Leu	Pro	Asp	Gly	Pro	Ala	Gly	Ser	Trp	65	70	75	80
Glu	Gln	Leu	Ile	Gln	Glu	Arg	Arg	Ser	His	Glu	Val	Asn	Pro	Ala	Ala	85	90	95	
His	Leu	Thr	Gly	Ala	Asn	Ser	Ser	Leu	Thr	Gly	Ser	Gly	Gly	Pro	Leu	100	105	110	
Leu	Trp	Glu	Thr	Gln	Leu	Gly	Leu	Ala	Phe	Leu	Arg	Gly	Leu	Ser	Tyr	115	120	125	
His	Asp	Gly	Ala	Leu	Val	Val	Thr	Lys	Ala	Gly	Tyr	Tyr	Tyr	Ile	Tyr	130	135	140	
Ser	Lys	Val	Gln	Leu	Gly	Gly	Val	Gly	Cys	Pro	Leu	Gly	Leu	Ala	Ser	145	150	155	160
Thr	Ile	Thr	His	Gly	Leu	Tyr	Lys	Arg	Thr	Pro	Arg	Tyr	Pro	Glu	Glu	165	170	175	
Leu	Glu	Leu	Leu	Val	Ser	Gln	Gln	Ser	Pro	Cys	Gly	Arg	Ala	Thr	Ser	180	185	190	
Ser	Ser	Arg	Val	Trp	Trp	Asp	Ser	Ser	Phe	Leu	Gly	Gly	Val	Val	His	195	200	205	
Leu	Glu	Ala	Gly	Glu	Glu	Val	Val	Val	Arg	Val	Leu	Asp	Glu	Arg	Leu	210	215	220	

Val Arg Leu Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
225 230 235 240

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Forward primer sequence

<400> 7

tatggattca tggaacctct cccaggat 28

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Backward primer sequence

<400> 8

tatggattcg gaggagcagg tgggtgtctgt 30

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Forward primer sequence

<220>
<221> misc_feature
<222> (17)...(17)
<223> N=Inosine

<400> 9

acgctggggc tggcctnctg a 21

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Backward primer sequence

<400> 10

actctcccat aacagcggcc

20

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Forward primer sequence

<220>
<221> misc_feature
<222> (10)...(10)
<223> N=Inosine

<400> 11

gagctggccn tgctgagggg cct

23

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Backward primer sequence

<400> 12

cagctgagtc tcccataaca

20

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Forward primer sequence

<220>
<221> misc_feature
<222> (7)...(7)
<223> N=Inosine

<400> 13

caggccntcc tgaggggcct ca 22

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Backward primer sequence

<400> 14

gcccagctga gtctcccata a 21

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Forward primer sequence

<400> 15

ttccccgagg agctggagct 20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Backward primer sequence

<400> 16

gcgggggtgtg cgcttgtaga

20
